

**FULL LISTING OF THE CURRENT PENDING CLAIMS**

1. **(Currently amended)** A method for identifying previously unidentified [[in]] diet-regulated disease-associated polynucleotides comprising the steps of:
  - (i) selecting a cohort from each of two different inbred rodent genotypes (A and B) all of the same generation and all either male or virgin female, one of these genotypes (A) being susceptible to a disease, and the other genotype (B) not susceptible to the same disease;
  - (ii) dividing each cohort into two groups (A1 and A2 and B1 and B2);
  - (iii) for each cohort, each group is fed a different diet (A1 is fed diet No. 1 and A2 is fed diet No. 2, and similarly for B1 and B2);
  - (iv) measuring gene expression and comparing expression across the individuals that differ in either genotype or in diet, but not in both;
  - (v) analyzing the expression data so as to identify in the disease-susceptible strain one or more genes that shows at least a two-fold increase or decrease in gene expression;
  - (vi) matching the genes shown above to have at least a two-fold increase or decrease in gene expression with one or more independently-derived quantitative trait loci (QTLs) known to encode one or more genes that contribute to the development of a disease,
  - (vii) wherein the genes so identified are considered to be a diet-regulated disease-associated genes.
- 2-3. **(Cancelled)**
4. **(Previously presented)** The method of claim 1 wherein gene expression is compared by comparing mRNA abundance.
- 5-16. **(Cancelled)**
- 17 **(Previously presented)** The method of claims 1 wherein gene expression is compared across individuals that differ in genotype only.

18. **(Previously presented)** The method of claim 1 wherein gene expression is compared across individuals that differ in diet only.
20. **(Currently amended)** The method of claim 1 wherein the one or more independently-derived quantitative trait loci is known to ~~eneede~~ be associated with one or more genes that contribute to diabetes.
21. **(Currently amended)** The method of claim 1 wherein the one or more independently-derived quantitative trait loci is known to ~~eneede~~ be associated with one or more genes that contribute to obesity.
22. **(Currently amended)** The method of claim 1 wherein the one or more independently-derived quantitative trait loci is known to ~~eneede~~ be associated with one or more genes that contribute to Alzheimer's disease.
23. **(Currently amended)** The method of claim 1 wherein the one or more independently-derived quantitative trait loci is known to ~~eneede~~ be associated with one or more genes that contribute to a cardiovascular disease.
24. **(Currently amended)** The method of claim 1 wherein the one or more independently-derived quantitative trait loci is known to ~~eneede~~ be associated with one or more genes that contribute to cancer.
25. **(Currently amended)** The method of claim 1 wherein the one or more independently-derived quantitative trait loci is known to ~~eneede~~ be associated with one or more genes that contribute to hypertension.